

## SEQUENCE LISTING

<110> Schopfer, Christel R  
 Flachmann, Ralf  
 Herbers, Karin  
 Kunze, Irene  
 Sauer, Matt  
 Klebsattel, Martin

<120> A process for preparing zeaxanthin and/or biosynthetic intermediates and/or secondary products thereof

<130> 13173-00001-US

<150> PCT/EP 03/009105

<151> 2003-08-18

<150> DE 102 38 980.2

<151> 2002-08-20

<150> DE 102 38 978.0

<151> 2002-08-20

<150> DE 102 38 979.9

<151> 2002-08-20

<150> DE 102 53 112.9

<151> 2002-11-13

<150> DE 102 58 971.2

<151> 2002-12-16

<160> 43

<170> PatentIn version 3.3

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<213> Arabidopsis thaliana

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<221> promoter

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ccaaacatta tctacaaaca aagacttttc tcttaacttg tgattccttc ttaaacccta 240

ggggtaatat tctattttcc aaggatcttt agttaaaggc aaatccggga aattattgta 300

atcatttggg gaaacatata aaagatttga gttagatgga agtgacgatt aatccaaaca 360

tatatatctc tttctttotta tttcccaaat taacagacaa aagtagaata ttggctttta 420

acaccaatat aaaaacttgc ttcacaccta aacacttttg tttacttttag ggtaagtgca 480  
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agaatcatta ctaacaatca atg agt atg aga gct gga cac atg acg gca aca      173
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atg gcg gct ttt aca tgc cct agg ttt atg act agc atc aga tac acg      221
Met Ala Ala Phe Thr Cys Pro Arg Phe Met Thr Ser Ile Arg Tyr Thr
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aag caa att aag tgc aac gct gct aaa agc cag cta gtc gtt aaa caa      269
Lys Gln Ile Lys Cys Asn Ala Ala Lys Ser Gln Leu Val Val Lys Gln
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gag att gag gag gaa gaa gat tat gtg aaa gcc ggt gga tcg gag ctg      317
Glu Ile Glu Glu Glu Glu Asp Tyr Val Lys Ala Gly Gly Ser Glu Leu
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ctt ttt gtt caa atg caa cag aat aag tcc atg gat gca cag tct agc      365
Leu Phe Val Gln Met Gln Gln Asn Lys Ser Met Asp Ala Gln Ser Ser
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cta tcc caa aag ctc cca agg gta cca ata gga gga gga gga gac agt      413
Leu Ser Gln Lys Leu Pro Arg Val Pro Ile Gly Gly Gly Gly Asp Ser
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aac tgt ata ctg gat ttg gtt gta att ggt tgt ggt cct gct ggc ctt      461
Asn Cys Ile Leu Asp Leu Val Val Ile Gly Cys Gly Pro Ala Gly Leu
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gct ctt gct gga gaa tca gcc aag cta ggc ttg aat gtc gca ctt atc      509
Ala Leu Ala Gly Glu Ser Ala Lys Leu Gly Leu Asn Val Ala Leu Ile
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ggc cct gat ctt cct ttt aca aat aac tat ggt gtt tgg gag gat gaa      557
Gly Pro Asp Leu Pro Phe Thr Asn Asn Tyr Gly Val Trp Glu Asp Glu
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Phe Ile Gly Leu Gly Leu Glu Gly Cys Ile Glu His Val Trp Arg Asp
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act gta gta tat ctt gat gac aac gat ccc att ctc ata ggt cgt gcc      653
Thr Val Val Tyr Leu Asp Asp Asn Asp Pro Ile Leu Ile Gly Arg Ala
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tat gga cga gtt agt cgt gat tta ctt cac gag gag ttg ttg act agg      701
Tyr Gly Arg Val Ser Arg Asp Leu Leu His Glu Glu Leu Leu Thr Arg
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tgc atg gag tca ggc gtt tca tat ctg agc tcc aaa gtg gaa cgg att      749
Cys Met Glu Ser Gly Val Ser Tyr Leu Ser Ser Lys Val Glu Arg Ile

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190	195	200	
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aca att cca tgc agg ctt gct act gtc gct tct gga gca gct tct gga Thr Ile Pro Cys Arg Leu Ala Thr Val Ala Ser Gly Ala Ala Ser Gly 220 225 230 235			845
aaa ctt ttg cag tat gaa ctt ggc ggt ccc cgt gtt tgc gtt caa aca Lys Leu Leu Gln Tyr Glu Leu Gly Gly Pro Arg Val Cys Val Gln Thr 240 245 250			893
gct tat ggt ata gag gtt gag gtt gaa agc ata ccc tat gat cca agc Ala Tyr Gly Ile Glu Val Glu Val Glu Ser Ile Pro Tyr Asp Pro Ser 255 260 265			941
cta atg gtt ttc atg gat tat aga gac tac acc aaa cat aaa tct caa Leu Met Val Phe Met Asp Tyr Arg Asp Tyr Thr Lys His Lys Ser Gln 270 275 280			989
tca cta gaa gca caa tat cca aca ttt ttg tat gtc atg cca atg tct Ser Leu Glu Ala Gln Tyr Pro Thr Phe Leu Tyr Val Met Pro Met Ser 285 290 295			1037
cca act aaa gta ttc ttt gag gaa act tgt ttg gct tca aaa gag gcc Pro Thr Lys Val Phe Phe Glu Glu Thr Cys Leu Ala Ser Lys Glu Ala 300 305 310 315			1085
atg cct ttt gag tta ttg aag aca aaa ctc atg tca aga tta aag act Met Pro Phe Glu Leu Leu Lys Thr Lys Leu Met Ser Arg Leu Lys Thr 320 325 330			1133
atg ggg atc cga ata acc aaa act tat gaa gag gaa tgg tca tat att Met Gly Ile Arg Ile Thr Lys Thr Tyr Glu Glu Glu Trp Ser Tyr Ile 335 340 345			1181
cca gta ggt gga tcc tta cca aat acc gag caa aag aac ctt gca ttt Pro Val Gly Gly Ser Leu Pro Asn Thr Glu Gln Lys Asn Leu Ala Phe 350 355 360			1229
ggt gct gct gct agc atg gtg cat cca gcc aca gga tat tcg gtt gta Gly Ala Ala Ala Ser Met Val His Pro Ala Thr Gly Tyr Ser Val Val 365 370 375			1277
aga tca ctg tca gaa gct cct aat tat gca gca gta att gca aag att Arg Ser Leu Ser Glu Ala Pro Asn Tyr Ala Ala Val Ile Ala Lys Ile 380 385 390 395			1325
tta ggg aaa gga aat tca aaa cag atg ctt gat cat gga aga tac aca Leu Gly Lys Gly Asn Ser Lys Gln Met Leu Asp His Gly Arg Tyr Thr 400 405 410			1373
acc aac atc tca aag caa gct tgg gaa aca ctt tgg ccc ctt gaa agg Thr Asn Ile Ser Lys Gln Ala Trp Glu Thr Leu Trp Pro Leu Glu Arg 415 420 425			1421
aaa aga cag aga gca ttc ttt ctc ttt gga tta gca ctg att gtc cag Lys Arg Gln Arg Ala Phe Phe Leu Phe Gly Leu Ala Leu Ile Val Gln			1469

430	435	440	
atg gat att gag ggg acc cgc aca ttc ttc cgg act ttc ttc cgc ttg			1517
Met Asp Ile Glu Gly Thr Arg Thr Phe Phe Arg Thr Phe Phe Arg Leu			
445	450	455	
ccc aca tgg atg tgg tgg ggg ttt ctt gga tct tcg tta tca tca act			1565
Pro Thr Trp Met Trp Trp Gly Phe Leu Gly Ser Ser Leu Ser Ser Thr			
460	465	470	475
gac ttg ata ata ttt gcg ttt tac atg ttt atc ata gca ccg cat agc			1613
Asp Leu Ile Ile Phe Ala Phe Tyr Met Phe Ile Ile Ala Pro His Ser			
480	485	490	
ctg aga atg ggt ctg gtt aga cat ttg ctt tct gac ccg aca gga gga			1661
Leu Arg Met Gly Leu Val Arg His Leu Leu Ser Asp Pro Thr Gly Gly			
495	500	505	
aca atg tta aaa gcg tat ctc acg ata taa ataactctag tcgcatcag			1711
Thr Met Leu Lys Ala Tyr Leu Thr Ile			
510	515		
tttagattat aggcacatct tgcatatata tatgtataaa ccttatgtgt gctgtatcct			1771
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Asn Ala Ala Lys Ser Gln Leu Val Val Lys Gln Glu Ile Glu Glu Glu			
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Glu Asp Tyr Val Lys Ala Gly Gly Ser Glu Leu Leu Phe Val Gln Met			
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Gln Gln Asn Lys Ser Met Asp Ala Gln Ser Ser Leu Ser Gln Lys Leu			
65	70	75	80
Pro Arg Val Pro Ile Gly Gly Gly Gly Asp Ser Asn Cys Ile Leu Asp			
85	90	95	
Leu Val Val Ile Gly Cys Gly Pro Ala Gly Leu Ala Leu Ala Gly Glu			
100	105	110	

Ser Ala Lys Leu Gly Leu Asn Val Ala Leu Ile Gly Pro Asp Leu Pro  
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Phe Thr Asn Asn Tyr Gly Val Trp Glu Asp Glu Phe Ile Gly Leu Gly  
 130 135 140

Leu Glu Gly Cys Ile Glu His Val Trp Arg Asp Thr Val Val Tyr Leu  
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Asp Asp Asn Asp Pro Ile Leu Ile Gly Arg Ala Tyr Gly Arg Val Ser  
 165 170 175

Arg Asp Leu Leu His Glu Glu Leu Leu Thr Arg Cys Met Glu Ser Gly  
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Val Ser Tyr Leu Ser Ser Lys Val Glu Arg Ile Thr Glu Ala Pro Asn  
 195 200 205

Gly Leu Ser Leu Ile Glu Cys Glu Gly Asn Ile Thr Ile Pro Cys Arg  
 210 215 220

Leu Ala Thr Val Ala Ser Gly Ala Ala Ser Gly Lys Leu Leu Gln Tyr  
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Glu Leu Gly Gly Pro Arg Val Cys Val Gln Thr Ala Tyr Gly Ile Glu  
 245 250 255

Val Glu Val Glu Ser Ile Pro Tyr Asp Pro Ser Leu Met Val Phe Met  
 260 265 270

Asp Tyr Arg Asp Tyr Thr Lys His Lys Ser Gln Ser Leu Glu Ala Gln  
 275 280 285

Tyr Pro Thr Phe Leu Tyr Val Met Pro Met Ser Pro Thr Lys Val Phe  
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Phe Glu Glu Thr Cys Leu Ala Ser Lys Glu Ala Met Pro Phe Glu Leu  
 305 310 315 320

Leu Lys Thr Lys Leu Met Ser Arg Leu Lys Thr Met Gly Ile Arg Ile  
 325 330 335

Thr Lys Thr Tyr Glu Glu Glu Trp Ser Tyr Ile Pro Val Gly Gly Ser  
 340 345 350

Leu Pro Asn Thr Glu Gln Lys Asn Leu Ala Phe Gly Ala Ala Ala Ser  
 355 360 365

Met Val His Pro Ala Thr Gly Tyr Ser Val Val Arg Ser Leu Ser Glu  
 370 375 380

Ala Pro Asn Tyr Ala Ala Val Ile Ala Lys Ile Leu Gly Lys Gly Asn  
 385 390 395 400

Ser Lys Gln Met Leu Asp His Gly Arg Tyr Thr Thr Asn Ile Ser Lys  
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Gln Ala Trp Glu Thr Leu Trp Pro Leu Glu Arg Lys Arg Gln Arg Ala  
 420 425 430

Phe Phe Leu Phe Gly Leu Ala Leu Ile Val Gln Met Asp Ile Glu Gly  
 435 440 445

Thr Arg Thr Phe Phe Arg Thr Phe Phe Arg Leu Pro Thr Trp Met Trp  
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Trp Gly Phe Leu Gly Ser Ser Leu Ser Ser Thr Asp Leu Ile Ile Phe  
 465 470 475 480

Ala Phe Tyr Met Phe Ile Ile Ala Pro His Ser Leu Arg Met Gly Leu  
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Tyr Leu Thr Ile  
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gaaaaagaat cattactaac aatcaatgag tatgagagct ggacacatga cggcaacaat 180  
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 gaaagccggt ggatcggagc tgctttttgt tcaaagcaa cagaataagt ccatggatgc 360  
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 <211> 446  
 <212> DNA  
 <213> tagetes erecta

<220>  
 <223> antisense fragment

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 ggcggctttt acatgcccta ggtttatgac tagcatcaga tacacgaagc aaattaagtg 240  
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 <211> 393  
 <212> DNA  
 <213> Tagetes erecta

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 <223> sense fragment

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 <211> 397  
 <212> DNA  
 <213> Tagetes erecta

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 <223> AntisenseFragment

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 gatagtaaaa tcgttagtta tgattaatac ttgggagggtg ggggattata ggctttgttg 420  
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attaaaataa agagaagaga aagattaaga gggatgatggg gatattaaag acggscaata	540
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tggtgcttaa tcaactcaac tcaactcata tcctatccat tcaaattcaa ttcaattcta	660
ttgaatgcaa agcaaagcaa aggttggttg ttggtgtgtg tgagagacac tccaatccaa	720
acagatacaa ggcg	734

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 <212> DNA  
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<220>  
 <223> variation

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tggttttaaa agatggcttg gctgctaata aactcaactc aactcatatc ctatccattc	180
aaattcaatt caattctatt gaatgcaaag caaagcaaag caaagggtgt ttggtgtgtg	240
tggtgagaga cactccaata caaacagata caaggcgtga	280

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 <211> 358  
 <212> DNA  
 <213> Tagetes erecta

<220>  
 <221> promoter  
 <222> (1)..(358)  
 <223> (sense) promotor

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tggagtttaa ttaaaataaa gagaagagaa agattaagag ggtgatgggg atattaaaga	180
cggccaatat agtgatgcca cgtagaaaaa ggtaagtga aacatacaac gtggctttaa	240
aagatggctt ggctgctaata caactcaact caactcatat cctatccatt caaattcaat	300
tcaattctat tgaatgcaaa gcaaagcaaa gcaaagggtg tttgtgtgtg ttgtcgac	358

<210> 14  
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 <212> DNA

<213> Tagetes erecta

<220>

<221> promoter

<222> (1)..(361)

<223> (antisense) promotor

<400> 14

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aaatggagtt taattaaaat aaagagaaga gaaagattaa gaggggtgatg gggatattaa      180
agacggccaa tatagtgatg ccacgtagaa aaaggtaagt gaaaacatac aacgtggctt      240
taaaagatgg cttggctgct aatcaactca actcaactca taccctatcc attcaaattc      300
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<220>

<223> Primer

<400> 15

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<220>

<223> Primer

<400> 16

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34

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<220>  
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25

<210> 19  
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<220>  
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<400> 19  
 gaaaatactt catcagcatt acc

23

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